

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 131974

TO: James Schultz

Location: rem/2d18/2c18

Art Unit: 1635

Wednesday, September 15, 2004 Case Serial Number: 10/019470 From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527



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.

From:

Schultz, James

Sent:

Wednesday, September 08, 2004 1:27 PM

To: Subject:

STIC-Biotech/ChemLib Seq Search 10/019,470

Hello.

Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?

Thanks,

Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

Searcher:______Searcher Phone: 2-Date Searcher Picked up:

STAFF USE ONLY

Date Completed: 9/15
Searcher Prep/Rev. Time:
Online Time:

Type of Search

Vendors and cost where applicable STN:
DIALOG:
QUESTEL/ORBIT:

QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
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Other(Specify):

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Minimum DB
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Listing first 45 summaries
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SUMMARIES

REFERENCE	SOURCE	AX096602 LOCUS DEFINITION ACCESSION VERSION	RESULT 1			4 4 4 3		4.4		د	ω	wu	c 33	w	30	c 29	ึงผ	26	N	0 0 223	N	N	۔ ر	18	17	c 15	<u>-</u> -	12	11	10	o 00	7 0	יט מ	י בי		, р	Result No.	1
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XESULT 1	
DEFINITION	1780 from Patent WO0118250.
ACCESSION	AX096602
VERSION	AX096602.1 GI:13512856
CEYWORDS	•
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and
	Mccarthy, J.J.
TITLE	Single nucleotide polymorphisms in genes

Pred. No. is the number of results predicted by chance to have a

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                      Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 1782 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH
Pharmaceuticals, Inc. (US)
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Sequence 1782 from Patent
AX096604
                                                                                  Lander, E.S.,
Mccarthy, J.J.
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patent: WO 0118250-A 1783 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH
Pharmaceuticals, Inc. (US)
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Sequence 1783 from Patent
AX096605
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                      1706 CCTCCGGGAACTCGCCAAGGT 1726
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Sequence 67 from Patent
AX153969
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Sequence 66 from Patent W00138576.
AX153968
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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95.2%;
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Pred. No. 9.1e+06;
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Pred. No. 9.1e+06;
1; Mismatches 0
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AX153971
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AX153970
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AX153971
  Homo
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Sequence 70 from Patent
AX153972
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Sequence 68 from Patent W00138576.
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Patent: WO 0138576-A 68 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        AX153972.1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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69 from Patent WO0138576.
                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 9.1e+06;
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Pred. No. 9.1e+06;
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AX153974
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Sequence 71 from Patent WO0138576.
AX153973
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Human single nucleotide polymorphisms
Patent: WO 0138576-A 70 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH
Location/Qualifiers
                          Cargill,M., Ireland,J.S. and Lander,E.S.
Human single nucleotide polymorphisms
Patent: WO 0138576-A 72 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
                                                                                                                                                                                         AX153974 21 bp
Sequence 72 from Patent WO0138576.
AX153974
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Human single nucleotide polymorphisms
Patent: WO 0138576-A 71 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH
                                                                                                                                Homo sapiens (human)
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
             Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 9.1e+06;
1; Mismatches (
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Pred. No. 9.1e+06;
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                                                                                                                 Euteleostomi;
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KEYWORDS
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AX458310/c
LOCUS
DEFINITION
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ORGANISM
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DEFINITION
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KEYWORDS
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AX791874
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Best Local Similarity
Matches 23; Conserv
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Sequence
AX791874
                                                                                                                                                                                                                                                                        27 bp
Sequence 5 from Patent EP1215214.
AX458310
                                                                                                                 Novel polypeptide
Patent: EP 1215214-A 5 19-JUN-2002;
Pfizer Limited (GB) ; PFIZER INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legrain, P., Rain, J.C., Colland, F., de Reuse, H. and Labigne, A. Protein-protein interactions in Helicobacter pylori Patent: Wo 02066501-A 4338 29-AUG-2002;
Hybrigenics (FR) ; INSTITUT PASTEUR (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
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Mammalia; Eutheria; Primates;
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Helicobacteraceae; Helicobacter.
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/mol_type="unassigned DNA"
/db_xref="taxon:210"
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Score 19.6; DB 6
Pred. No. 1.5e+07
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RESULT 15
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AUTHORS
TITLE
JOURNAL
Search completed: September 15, 2004, 10:39:44 Job time : 10903 secs
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                                                                                                                                             Query Match 0.7%; Score 19.6; DB 6; Length 27; Best Local Similarity 84.6%; Pred. No. 1.5e+07; Matches 22; Conservative 0; Mismatches 4; Indels
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S JP 2003009885-A/3.

S JP 2003009885-A/3.

Homo Sapiens (human)

ISM Homo Sapiens (substance)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 27)

RS Fidock,M.D.

Novel polypeptide

Patent: JP 2003009885-A 3 14-JAN-2003;

Pfizer Ltd (EP(GB) only), Pfizer Inc (US JP EP except GB)

OS Homo Sapiens

PN JP 2003009885-A/3

PD 14-JAN-2003

PF 17-DEC-2001 JP 2001382707

PR 18-DEC-2001 GB 0030855.1,17-JAN-2001 GB 0101222.8 PI

mark david fidock

CC

FH Key Tocation/Qualifiers.
                                                                                            1415 GGAAGGAAGCAAAAGGATCAACATGG 1440
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Novel polypeptide.
BD187418
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Location/Qualifiers.
1...27
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/mol_type="genomic DNA"
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                              Database
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                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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seq length: 30
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11409.216 Million cell updates/sec
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1 gttgaaagctcct
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1: geneseqn1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2221115	No.	
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Aai Aal Aal Aal Aal Aal Aal Aal Aaa Aaa Aaa	Des Aaa Aaa Aaa Aaa Aaa	
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Human gen Human gen Phosphory Human liv	ion Human Human Human Human Human Human Human Human	
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Antisense compounds particularly oligonucleotides useful for prophylaxis, diagnosis and treatment of diseases associated with expression of liver glycogen phosphorylase.

Example 13; Col 38; 33pp; English.

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0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
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Aaa14032 Human liv	Human	Aaa14013 Human li	Aaa14038 Human li	Aaa14021 Human li	Aaa14035 Human li	Aaa14031 Human li	Aaa14024 Human liv	Aaa14016 Human liv	Aaa14014 Human liv	Aaa14040 Human liv	Aaa14028 Human li	Aaa14033 Human liv	Aaa14019 Human li	Aaa14036 Human liv	Aaa14026 Human liv	Aaa14022 Human li	Aaa14012 Human li	Aaa14009 Human li	Aaa14008 Human liv	Aaa14015 Human liv
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ALIGNMENTS

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RESULT 1
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                                                                                                                                                                                                               WPI; 2000-270346/23.
                                                                                                                                                                                                                                                                                      Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1999;
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/note= "Conjugated to fluorescent reporter dye FAM"
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RESULT 2
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AC AAA140
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XX Liver
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KW 91ycog
KW expres
KW type 1
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human liver glycogen phosphorylase probe used CC in quantitative real-time PCR with primers AAA14002-A14003 in an CC exemplification of the present invention. The invention relates to CC antisense oligonucleotides targetted to the human liver glycogen CC cligonucleotides (AAA14008-A14040), which inhibit its expression. A series of CC oligonucleotides (AAA14008-A14040), which inhibit its expression. A series of cligonucleotides (AAA14008-A14040) were designed to target different cregions of human liver glycogen phosphorylase levels by quantitative real-time pCR. GAPDH (glycoraldehyde-3-phosphorylase levels by quantitative real-time pCR. GAPDH (glycoraldehyde-3-phosphorylase lavels were measured as a control liver glycogen phosphorylase is one of three glycogen phosphorylase is one of three glycogen glosphorylase is one of three glycogen phosphorylase is one of three glycogen coditions, immunological properties and electrophoretic mobilities and cleared by the PVGI gene, which is located on chromosome 14. Liver glycogen phosphorylase (also known as 1.4-alpha-D-glucan:orthophosphate coded by the PVGI gene, which is located on chromosome 14. Liver glycogen phosphorylase (also known as 1.4-alpha-D-glucan:orthophosphate coded by the pVGI gene, which is located on chromosome 14. Liver coded codes and creation of stored glycogen in the liver to glucose-1-phosphate via the cleavage of the alpha-1,4-glycogidic bonds. It therefore plays a critical role in carbohydrate metabolism and blood glucose homeostasis. Inhibition of stored glycogen phosphorylase and therefore glycogen phosphorylase and creations of reducing blood glucose levels in diabetes. The antisense oilgonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                          WPI; 2000-270346/23
                                                                                                                                               Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression inhibition; antisense therapy type II diabetes; non insulin-dependent; quantitative real-time PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa; glycogenolysis; carbohydrate metabolism; blood glucose homeostasis; expression inhibition; antisense therapy; hypoglycaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 BP; 5
                                                                                                                                                                                                                                                                                                                      19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6043091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human liver glycogen phosphorylase quantitative real-time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA14003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA14003 standard; DNA; 21
                                                                                                                                                                                                                                (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liver glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 CTGTGATGAGGCCATTTACCAGCTTGG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTGATGAGGCCATTTACCAGCTTGG 27
                                                                                                                                           Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorylase; PYGL gene; human; chromosome 14;
                                                                                                                                                                                                                                                                                                                      99US-00357071.
                                                                                                                                                                                                                                                                                                                                                                                                           99US-00357071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        쁑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ģ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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S

glycogen phosphorylase. Antisense compounds particularly oligonucleotides useful for prophylaxis, diagnosis and treatment of diseases associated with expression of liver

Example 13; Col 38; 33pp; English.

cc phosphorylase gene (PyGL gene), which inhibit ite expression. A series of cligonucleotides (AAA14008-A14047) were designed to target different cc regions of human liver glycogen phosphorylase RNA, and were analysed for their effect on liver glycogen phosphorylase RNA, and were measured as control. Liver glycogen phosphorylase levels by quantitative real-cc time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as control. Liver glycogen phosphorylase is one of three glycogen phosphorylase is one of three glycogen phosphorylase is one of three glycogen cc phosphorylase isogen; which differ in their tissue-specific cc encoded by three different genes. Liver glycogen phosphorylase is cc encoded by the PYGL gene, which is located on chromosome 14. Liver cc glycogen phosphorylase (also known as 1.4-alpha-0-glucan:orthophosphate cc form) catalyses the degradation of stored glycogen in the liver to glycogen phosphorylase (also known as 1.4-alpha-0-glucan:orthophosphate cc form) catalyses the degradation of stored glycogen in the liver to glycose-1-phosphate via the cleavage of the alpha-1,4-glycogidic bonds. Cc therefore glays a critical role in carbohydrate metabolism and blood glucose homeostasis. Inhibition of liver glycogen phosphorylase and creatment of conditions associated conseinl for diagnosis, prevention and treatment of conditions associated conseinl for diagnosis, prevention and treatment of conditions associated control inhibition of liver glycogen phosphorylase expression, or those which may benefit crom inhibition of liver glycogen phosphorylase expression, such as type cc II diaheten FCK primers used in quantitative real-time PCR with probe AAA140 exemplification of the present invention. The invention relates antisense oligonucleotides targetted to the human liver glycogen the probability of the probe with the probe and the probability of II diabetes Sequences AAA14002-A14003 represent human liver glyce PCR primers used in quantitative real-time PCR with AAA14002-A14003 represent human liver glycogen phosphorylase AAA14003 6 in an

Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Ś Query Match Best Local Matches 505 21; Similarity GACTTGGCAATGGTGGTCTTG Conservative 100.0%; 0 Score 21; Pred. No. 525 Mismatches DB 3; L 1.2e+05; 0; Indels Length 21 0 Gaps 0

AAA14002 standard; DNA; 21

片

22

GACTTGGCAATGGTGGTCTTG

ш

AAA14002

18-JUL-2000

(first

entry)

Human liver glycogen phosphorylase quantitative real-time PCR primer #2

RESULT 3
AAA1402
ID AAAA1
XX AAA1
AC AAA1
XX Live
DT 18-J
XX Live
KW Live
KW 1,4
KW 1,4
KW expp
KW expp
KW expp
KW expp
KW exp
K 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; glycogenolysis; carbohydrate metabolism; blood glucose homeoste expression inhibition; antisense therapy; hypoglycaemic; type II diabetes; non insulln-dependent; 19-JUL-1999; 28-MAR-2000 US6043091-A Homo quantitative real-time PCR primer; Liver glycogen phosphorylase; PYGL gene; human; chromosome 14; 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; 19-JUL-1999; sapiens 9908-00357071. 99US-00357071. homeostasis; HGLPa;

(ISIS-) ISIS

PHARM INC

Monia

B₽,

Cowsert

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ARESULT 4
AAP97019
ID AAP9
XX AAP9
XX AAP9
XX Huma
XX Huma
XX Huma
XX Huma
XX myoc
KW polly
KW myoc
XX Hom

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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate alpha-D-glucoan; orthophosphate alpha-D-glucoan; orthophosphate alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active form) catalyses the degradation of stored glycogen in the liver to glucose-l-phosphate via the cleavage of the alpha-1,4-glycosidic bonds. It therefore plays a critical role in carbohydrate metabolism and blood glucose homeostasis. Inhibition of liver glycogen phosphorylase and therefore glycogenolysis may provide a means of reducing blood glucose levels in diabetic patients, particularly those with type II (non insulin dependent) diabetes. The antisense oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with liver glycogen phosphorylase expression, or those which may benefit from inhibition of liver glycogen phosphorylase expression, such as type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primers used in quantitative real-time PCR with probe AAA14003 in an exemplification of the present invention. The invention relates to antisense oligonucleotides targetted to the human liver glycogen phosphorylase gene (PYGL gene), which inhibit its expression. A series of oligonucleotides (AAA14008-A14047) were designed to target different regions of human liver glycogen phosphorylase RNA, and were analysed for their effect on liver glycogen phosphorylase levels by quantitative real-time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as control. Liver glycogen phosphorylase is one of three glycogen phosphorylase is organized, which differ in their tissue-specific distribution, immunological properties and electrophoretic mobilities and are encoded by three different genes. Liver glycogen phosphorylase is encoded by the PYGL gene, which is located on chromosome 14. Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycogen phosphorylase.
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                                                                                                                                                                                                                                                                                                                                                             Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forens myocardial infarction; atherosclerosis; stroke; venous thromboe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene single nucleotide polymorphism #1780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAA14002-A14003 represent human liver glycogen phosphorylase PCR primers used in quantitative real-time PCR with probe AAA14003 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 13; Col 38; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF97019 standard; DNA; 21 BP
       WO200118250-A2
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                           pulmonary embolism;
                                                                                                                                                Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 CATGGGCCGAACATTACAGAA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                         Location/Qualifiers replace(11,G)
                                                                      /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;
                                                                                                                                                                                                                                                                                                                           paternity test;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 3; Length 21; Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                           ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                e; forensics;
thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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RESULT 5
AAP97017
ID AAP9
XX AAP9
XX AAP9
XX Huma
AC Huma
XX Huma
XX M Myoc
KW Myoc
KW Myol
KW
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thrombosembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                              Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21
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26-JUL-2000; 2000US-0220947P.
16-AUG-2000; 2000US-0225724P.
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     pulmonary embolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene single nucleotide polymorphism #1778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF97017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF97017 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 166; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerosis.
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                                                             15-MAR-2001.
                                                                                                                        WO200118250-A2
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                                                                                                                                                                                                                                                                                                                                                                                        paternity test; ds.
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Pred. No.
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hes 0;
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07-SEP-2000; 2000WO-US024503.

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RESULT 6
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XX Huma
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Matches 21
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26-JUL-2000;
16-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembol pulmonary embolism; paternity test; ds.
                                                                                                          07-SEP-2000;
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2000US-0220947P.
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1.2e+05;
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16-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forens myocardial infarction; atherosclerosis; stroke; venous thromboe pulmonary embolism; paternity test; ds.
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                          (WILL-)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                                                                             Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Page 166; 242pp;
                                                                                                                                                                                                                                                                                                                                                                                                Human gene single nucleotide polymorphism #1779.
                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF97018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF97018 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 6 A; 7 C; 3
                                                                                                                    26-JUL-2000;
                                                                                                                               10-SEP-1999;
                                                                                                                                                          07-SEP-2000; 2000WO-US024503
                                                                                                                                                                                     15-MAR-2001.
                                                                                                                                                                                                              WO200118250-A2
                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                 pulmonary embolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the human gene SNPS shown in the specification
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                                                                                                                                                                                                                                                                  Variation
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                                                               WHITEHEAD INST BIOMEDICAL MILLENNIUM PHARM INC.
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                                     Gargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                     99US-0153357P.
2000US-0220947P.
2000US-0225724P.
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                                                                                                                                                                                                                                    replace(11,G)
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100.0%; Pr
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                                      Ireland
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                                                                                                                                                                                                                                      polymorphism"
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                                      Mccarthy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart diagnosis of atherosclerosis, myocardial infarction, coronary heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids comprising single nucleotide polymorphisms, useful applications such as forensics, paternity testing, medicine, gene analysis and phenotype correlations to diseases such as diabetes atherosclerosis.
                                                                                                                                                              New nucleic acid segments of the human genome, particularly including polymorphic sites, for phenotype correlation, forer paternity testing, medicine and genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1999;
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                                                                                                                                                                                                                                                                                   2001-367705/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
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DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of

Claim

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English.

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Query Match
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Matches 21
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                                            determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in
     applications
medicine and
                                                                                                                                                                                                                                        DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of
                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid segments of the human genome, particularly from including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis.
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                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 35; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-367705/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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such as phenotype genetic analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "single nucleotide polymorphism"
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                              correlation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                              forensics, paternity testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                  genes which
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2269 TGGCTGCTTTGGACAAGAAAG 2289

Query Match Best Local S Matches 21

Similarity

0.7%;

Score 21; ; Pred. No.

Conservative

<u>,,</u>

Mismatches

1.2e+05; DB 4;

Indels

0

Gaps

0,

Length 21;

Sequence

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RESULT 11
AAH62169
ID AAH622
XX AAH62
XX Phosp
XX Singl
XW Singl
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XX Ho
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Best Local Simi
Matches 21;
                                               DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the disgnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid segments of the human genome, particularly from including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 35; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism; SNP; human; cancer; heart disease; paternity testing; forensic science;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylaes glycogen polymorphism containing DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH62169 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2279 GGACAAGAAAGGGTACGAGGC 2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease;
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     21
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Conservative
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  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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  6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(11,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/standard_name=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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  3 C; 7 G;
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Pred. No.
  5 T;
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     0 U; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2e+05
     Other;
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ARBSULT 12
AAH62167
ID AAH62
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XX Phosp
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CO Homo
XX Hom
RESULT 13
AAH62171
ID AAH62
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AC AAH62
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPP). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis
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                            AAH62171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 34; 80pp;
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                                                                                         AAH62171 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                       2003 GGTGAACAATGACCCTATGGT 2023
                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                GGTGAACAATGACCCTATGGT 21
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                          0.7%; 500
100.0%; Pr
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 21; 1.2e+05;
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AAH62166
II AAHH
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AC AAHE
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AC AAHE
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DT 12-5
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DE Phos
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KW Sing
KW Sing
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OS Homm
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                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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Best Local (
                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single nucleotide polymorphism; SNP; human; cancer; inf heart disease; paternity testing; forensic science; ds.
                Homo sapiens
                                             Single nucleotide polymorphism; SNP; human; cancer; heart disease; paternity testing; forensic science;
                                                                                           Phosphorylaes glycogen polymorphism containng DNA fragment #67.
                                                                                                                            12-SEP-2001
                                                                                                                                                           AAH62166
                                                                                                                                                                                      AAH62166 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 35; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
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                                                                                                                                                                                                                                                                                                  2350 TTGACAATGGCTTTTTTCTC 2370
                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                                            BP; 3 A; 4 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ireland JS,
                                                                                                                                                                                                                                                                                                                                 Conservative
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Variation
                                                  31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylaes glycogen polymorphism containing DNA fragment #69.
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Search completed: September 15, Job time: 1054 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis.
                                                                                                                                                                                                                                                           applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                              contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequences AAH62100 - AAH62688 represent segments of human genes which
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Sequence 28, Appl	Sequence 11, Appl	Sequence 47, Appl	Sequence 46, Appl	Sequence 45, Appl	Sequence 44, Appl	-	•	•	Sequence 40, Appl	•	Sequence 38, Appl	Sequence 37, Appl	•	•	Sequence 34, Appl	Sequence 33, Appl	Sequence 32, Appl

Sequence 4, Application US/09357071 Patent No. 6043091

ALIGNMENTS

GENERAL INFORMATION:
APPLICANT: Breet P. Monia
APPLICANT: Lex M. Cowsert
APPLICANT: LOS M. COWSERT
TITLE OF INVENTION: ANTIJENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REFERENCE: RTS-0074
CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence

; OTHER INFORMATION: PCR Probe US-09-357-071-4 100.0%; 1.0%; Score 27; Pred. No. DB 3; 2.9e+0

.9e+02

Gaps

0

Length 27;

437 CTGTGATGAGGCCATTTACCAGCTTGG 463 1 CTGTGATGAGGCCATTTACCAGCTTGG 27 <u>.</u> Mismatches 0 Indels 0

; FEATURE: ; OTHER INFORMATION: PCR Primer US-09-357-071-2 Sequence 2, Application US/09357071

Patent No. 6043091

GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REFERENCE: RTS-0074

CURRENT APPLICATION NUMBER: US/09/357,071

CURRENT FILING DATE: 1999-07-19 NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
LENGTH: 21
TYPE: DNA Query Match ORGANISM: Artificial Sequence 0.7%; Score 21; В ω --Length 21;

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                                                                                     RESULT 5
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Patent No. 6043091
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REFERENCE: RTS-0074
CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
                        Sequence 9, Application US/09357071
Patent No. 6043091
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 8
LENGTH: 20
LENGTH: 20
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Patent No. 6043091
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. COWBERT
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER
FILE REFERENCE: RTS-0074
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SEQ ID NO 3
LENGTH: 21
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APPLICANT:
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Lex M. Cowsert
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; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-11
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US-09-357-071-10
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Best Local S
Matches 20
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Best Local S
Matches 20
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APPLICANT: LEX M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0074
CURRENT EPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                      Sequence 11, Application US/09357071 Patent No. 6043091 GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0074
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LENGTH: 20
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SEQ ID NO 9
Query Match
Best Local Similarity
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CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
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CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
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                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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US-09-357-071-12/c
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Patent No. 6043091

GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. COWSERT

TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REFERENCE: RTS-0074

CURRENT APPLICATION NUMBER: US/09/357,071

CURRENT FILING DATE: 1999-07-19
Sequence 14, Application US/09357071
Patent No. 6043091
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 13
LENGTH: 20
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Patent No. 6043091
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Coweert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER
FILE REFERENCE: RTS-0074
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Best Local Similarity
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TYPE: DNA
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US-09-357-071-16/c
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US-09-357-071-15/c
                                                             ; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-16
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LENGTH: 20
TYPE: DNA
Query Match
Best Local S
Matches 20
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APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09357071 Patent No. 6043091
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0074
CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
                                                                                                                                                                                                                        APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0074
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                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20
TYPE: DNA
                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                FEATURE:
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                                                                                                                                             LENGTH: 20
y Match 0.7%; S
Local Similarity 100.0%; hes 20; Conservative 0;
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00.0%; Pred. No.
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Score 20; DB; Pred. No. 2.2 0; Mismatches
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                DB 3; L
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2.2e+04;
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TCTCTGGAATTTTACATGGG 391

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RESULT 15
US-09-357-071-19/c
; Sequence 19, Application US/09357071
; Patent No. 6043091
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SEQ ID NO 18
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-09-357-071-17/c
; Sequence 17, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
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US-09-357-071-18/c
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APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REPERENCE: RTS-0074
CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
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APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REPERENCE: RTS-0074
CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 17
LENGTH: 20
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REFERENCE: RTS-0074
                                                                                                                                                                                                                                                                                Query Match 0.7
Best Local Similarity 100
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Conservative (
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100.0%; Pred. No. 2.2e+04
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Search completed: September 15, 2004, 12:40:24 Job time : 195 secs
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                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 19
LENGTH: 20
                                                                                                                                                              Query Match 0.7%; Score 20; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Post-processing: Minimum Match 0%
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Perfect score:
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seq length: 30
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9C_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9C_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9NEW_PUB.seq:*
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US-10-114-544-4
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US-10-114-544-8
US-10-114-544-9
US-10-114-544-10
US-10-114-544-11
US-10-114-544-13
US-10-114-544-14
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ALIGNMENTS

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Sequence 4, Application US/10114544

Publication No. US20030166592A1

GENERAL INFORMATION:
APPLICANT: Exett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTSP-0240

CURRENT APPLICATION NUMBER: US/10/114,544

CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 4
LENGTH: 27
                                                                                                                                                    Ś
                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE: OTHER IMPORMATION: PCR Probe US-10-114-544-4
                        RESULT 2
US-10-114-544-2
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US-10-114-544-4
; Sequence 2, Application US/10114544
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Best Local
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00.0%; Pred. No. 1.2e+03;
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Publication No. US20030166592A1

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FILE REFERENCE: RTSP-0240
CURRENT APPLICATION NUMBER: US/10/114,544
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 199-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
LENGTH: 21
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                                                             Sequence 8, Application US/10114544 Publication No. US20030166592A1 GENERAL INFORMATION:
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SEQ ID NO 3
LENGTH: 21
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Publication No. US20030166592A1
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CURRENT APPLICATION NUMBER: US/10/114,544
CURRENT FILING DATE: 2002-04-01
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TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
TITLE OF INVENTION: EXPRESSION
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
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TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
TITLE OF INVENTION: EXPRESSION
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APPLICANT: Lex N
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: PCR Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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les 21; Conservative
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100.0%; Pr
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US-10-114-544-10/c
Sequence 10, Application US/10114544
Publication No. US20030166592A1
GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
APPLICANT: Lex M. Cowsert TITLE OF INVENTION: EXPRESSION FILE OF INVENTION: EXPRESSION FILE REFERENCE: RTSP-0240 CURRENT APPLICATION NUMBER: US/10/114,544 CURRENT FILLING DATE: 2002-04-01 PRIOR APPLICATION NUMBER: 10/019,470
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CURRENT FILLIG DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
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                                                                                                              APPLICANT: Brett APPLICANT: Lex N
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CURRENT FILING DATE: 2002-04-01
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L00.0%; Pred. No.
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09/357,071

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NUMBER OF SEQ ID NOS: 47
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-10-114-544-11/c
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APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
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Publication No. US20030166592A1
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Best Local Similarity
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                       APPLICANT: Brett P. Monia
APPLICANT: Lex M. COWSETT
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTSP-0240
CURRENT APPLICATION NUMBER: US/10/114,544
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
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CURRENT APPLICATION NUMBER: US/10/114,544
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS:
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; Pred. No. 1.2e+05;
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/114,544

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 10/019,470

PRIOR FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: US 09/357,071

PRIOR FILING DATE: 1999-07-19

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PRIOR FILING DATE: 1999-07-19
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                                                                           SEQ ID NO 14
LENGTH: 20
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Best Local Similarity
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Best Local Similarity
                                                                                                                               CURRENT APPLICATION NUMBER: US/10/114,544
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTISENSE MODULATION TITLE OF INVENTION: EXPRESSION FILE REFERENCE: RTSP-0240
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                                                                                                                   NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                         APPLICANT: Brett P. Monia APPLICANT: Lex M. Cowsert
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TYPE: DNA
ORGANISM: Artificial Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
                                     ORGANISM: Artificial Sequence
                                                           TYPE: DNA
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|00.0%; Pred. No. 1.2e+0!
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FILE REFERENCE: RTSP-0240
CURRENT APPLICATION NUMBER: US/10/114,544
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 15
LENGTH: 20
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US-10-114-544-16/c
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                                                                                                                                                                                                                                                                                 Sequence 16, Application US/10114544
Publication No. US20030166592A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTSP-0240
CURRENT APPLICATION NUMBER: US/10/114,544
CURRENT FILING DATE: 2002-04-01
PRICE ADDITORNIA NUMBER: 2002-04-01
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SEQ ID NO 16
LENGTH: 20
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Publication No. US20030166592A1
                  Best Local Similarity
                                 Query Match
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APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
                                                                                        OTHER INFORMATION: Antisense Oligonucleotide
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Score 20; DB 15;
; Pred. No. 1.2e+05;
0; Mismatches 0;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-18
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US-10-114-544-18/c
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US-10-114-544-17/c
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Publication No. US20030166592A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/10114544 Publication No. US20030166592A1 GENERAL INFORMATION:
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LENGTH: 20
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Best Local Similarity
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CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/357,071
PRIOR FILING DATE: 1999-07-19
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CURRENT APPLICATION NUMBER: US/10/114,544

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 10/019,470

PRIOR FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: US 09/357,071

PRIOR FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE TITLE OF INVENTION: EXPRESSION FILE REFERENCE: RTSP-0240
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APPLICANT: Lex M
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TYPE: DNA
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ative 0; Mismatches
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US-10-114-544-19/c

Sequence 19, Application US/10114544

Publication No. US20030166592A1

GENERAL INFORMATION: Monia
APPLICANT: Exet P. Monia
APPLICANT: Lex M. Cowsert
ITILE OF INVERTION: EXPRESSION
FILE REFERENCE: RTSP-0240

CURRENT APPLICATION NUMBER: US/10/114,544

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 10/019,470
PRIOR APPLICATION NUMBER: 10/019,470
PRIOR FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: US 09/357,071

PRIOR APPLICATION NUMBER: US 09/357,071

PRIOR FILING DATE: 1999-07-19

SEQ ID NO 19

CRANNISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

US-10-114-544-19

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy

523 TTGGGAGACTTGCTGCTGC
Qy

Search completed: September 15, 2004, 13:01:36

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

n		Ω		Result No.
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0.6	0.6	0.6	0.6	Query Match Length DB
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ALIGNMENTS

	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AZ782046 LOCUS DEFINITION
University of Utah University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177	Diasmid inserts Unpublished (2000) Contact: Robert B. Weiss	Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb	1 (bases 1 to 28) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam.H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	AZ782046	AZ782046 28 bp DNA linear GSS 16-FEB-2001 200021N19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

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SOURCE
ORGANISM
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AZ514403/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 bp DNA linear GSS 05 1M0361K06F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0361K06 F, genomic survey sequence. AZ514403
                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                 plasmid inserts
Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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High quality sequence stop: 29.
Location/Qualifiers
                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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AZ990068.1 GI:13861295
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2M0273G07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0273G07 R, genomic survey sequence.
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19; Conservative
801 585 5606
801 585 7177
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/strain="C57BL/6J"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Tnsert Length: 10000 Std Error:
                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C5PBL/6J (Female) was obtained from the Jackson
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/strain="C57BL/6J"
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CF305882
CF305882.1
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Obp mRNA linear EST 15-AUG-2003 HDA1--02-A08.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--02-A08, mRNA
                                                                                                                                                                                         Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
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Location/Qualifiers
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Plate: 0059 ro
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Insert Length: 10000 Std Error: 0.00
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                              Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                      of Bioscience and Bioinformatics,
                                                                                                                                                   Genomics and Genetics Institute,
                                                                                                                                                                          Contact: Nahm B.H
                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="g. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMB42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone="UUGC1M0059L06"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                            bhnahm@bio.myongji.ac.kr
                                                                                                                         GreenGene Biotech II
, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6,
                                                                                                                                                                                                                                                                          Lee, T.H.,
                                                                                                                                                     Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 29;
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CC458485/c
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ORGANISM
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 CTGCGGGTGTGCTCCTGTTGGGGCGCTGG 2
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SALK_119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
CC458485
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                                                                                                                                                                                                                                                                                                                                                                                                                  This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g55380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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119217.40.80.x Arabidopsis thaliana TDNA insertion lines
idopsis thaliana genomic clone SALK_119217.40.80.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                TDNA tagged.
Location/Qualifiers
                            /clone="SALK 119217.40.80.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBiuescript SK(+); Site 1: EcoRI; Site 2: XhoI, Callus was treated with ABA(20um) for Thour. CDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phage cDNA library I (HDA1)
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/lab_host="E.coli SOLR"
/clone_lib="09HDAC1-overexpressing transgenic rice lambda
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
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/tissue_type="callus"
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                                                                                                                                                                                                                                       _xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                           2633 ATCTAACAAAGTCAATGGAAATTG 2656
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                                                                                                                                                                       BH908631 26 bp DNA linear GSS SALK 049758.30.10.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 049758.30.10.x,
                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                              Arabidopsis thaliana
                                                                                                              BH908631.1 GI:22721564
GSS.
                                                                                                                                            вн908631
                                                                                                                                                                                                                                                                                            2 ATCANAGANAGTTTATGANATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute for Molecular and Cellular Biology Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression Nat. Genet. 2, 173-179 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                           survey sequence.
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Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 26)
1 (bases 1 to 26)
Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y.
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D11539.1 GI:511920
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                                                                                               Arabidopsis thaliana (thale cress)
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                (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada-oka, Suita, Osaka 565, Japan.
                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Liver HepG2 cell line./note="3'-directed regional cDNA and transformed into E.coli."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:DOS8041E"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="c12b04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'lab_host="E.coli"
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Leisse, T.J., Barajas, P.,
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3.5e+07;
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   Chen, H.,
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   Cheuk, R.
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
Contact: Joneth 1
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AL464342
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                                                                                        to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                                                                                                                                                                                                                                                                                                                                                                                                                Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                        nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 858 558 6379
                                                                              Barrell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="SALK_049758.30.10.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                              Oxford University Press,
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/strain="Columbia 0"
/db_xref="taxon:3702"
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Pred. No. 3.5e+07;
0; Mismatches 5
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0554 row: C column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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AZ760461.1 GI:12868327
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clone UUGC1M0554C13 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org//esources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg.,
                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
Laboratory Mouse DNA Resource
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/strain="TREU927"
/db_xref="taxon:5691"
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/strain="C57BL/6J"
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'clone="UUGC1M0554C13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R. Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 10000 Std Error: (Plate: 0045 row: A column: 07 Seq primer: CACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 29.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
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Fax: 801 585 7177
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                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /Clone lib="Mouse 10kb plasmid UUGC1M library /note="Vector: PW042nv; purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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crophoresis. Vector DNA was prepared fr
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Pred. No. 3.6e+07;
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0535 row: M column: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
High quality sequence stop:
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
                                                                                                                                                                                                                                                       /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: P column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
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/strain="C57BL/6J"
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Mus musculus (house mouse)
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Population analysis of CDNAs from unicellular and multicellular
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University of Tsukuba
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                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Dictyostelium
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                   /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                       /sex="mat A"
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0220 row: E column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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'clone="UUGC1M0220E07"
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